



Supplementary Figure 3. A broad range of reads originates from rRNAs in haustoria and microsomal fractions. (A) We aligned all reads to the 5.8S (red), 18S (blue), and 28S (green) rDNA sequences of *B. hordei* and *H. vulgare*. The stacked bar graph shows the read counts (y-axis) for the respective read size (x-axis) from the three replicates. Three replicates were analyzed for each of our six sample types: Epiphytic fungal mycelium (MYC), infected epidermis without mycelium (EPI), fungal haustoria (HAU), microsomes of the epidermis without haustoria (P40), apoplastic extracellular vesicles (EV+), and apoplastic extracellular vesicles of non-infected control plants (EV-). Colors indicate reads aligning to the different rDNAs: Light blue, *B. hordei* 18S rDNA (RNAcentral accession URS000021D3E6_2867405); dark blue, *H. vulgare* 18S rDNA (URS0000AF30DE_112509); light green, *B. hordei* 28S rDNA (URS0002174482_62688); dark green, *H. vulgare* 28S rDNA (URS000212856A_112509); light red, *B. hordei* 5.8S rDNA (URS00006663F0_546991); dark red, *H. vulgare* 5.8S rDNA (URS0000C3A4AE_112509); grey, reads that did not align with any rDNA sequence. **(B)** Alignment of sRNA sequencing reads of 27-32 bases in length from HAU to the *B. hordei* 5.8S rDNA (154 bases in length). The graph shows the cumulative number of reads from the three replicates (y-axis) mapping to each position of the *B. hordei* 5.8S rDNA (x-axis). **(C)** Secondary structure of the *B. hordei* 5.8S rRNA (RFAM accession CAUH01009408.1:1222-1375; RNA central accession URS00006663F0_546991) predicted by R2DT in RNA central (<https://rnacentral.org>) and visualized with Forna (Kerpedjiev *et al.* 2015). The RNA sequences in orange indicates the over-represented 3' end in the reads from the HAU sample.